



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/501,671
Source: PG/10
Date Processed by STIC: 7/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S.; Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/501,671</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



PCT

RAW SEQUENCE LISTING

DATE: 07/23/2004

PATENT APPLICATION: US/10/501,671

TIME: 15:23:45

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07232004\J501671.raw

3 <110> APPLICANT: Asahi Kasei Kabushiki Kaisha
W--> 4 <120> TITLE OF INVENTION: High-concentration preparation of soluble thrombomodulin
6 <130> FILE REFERENCE: ASAHI-33
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/501,671
C--> 8 <141> CURRENT FILING DATE: 2004-07-16
8 <150> PRIOR APPLICATION NUMBER: JP2002-009951
9 <151> PRIOR FILING DATE: 2002-01-18
11 <160> NUMBER OF SEQ ID NOS: 9

ERRORED SEQUENCES

13 <210> SEQ ID NO: 1
14 <211> LENGTH: 516
15 <212> TYPE: PRT
16 <213> ORGANISM: Artificial sequence
18 <220> FEATURE:
19 <223> OTHER INFORMATION: Partial amino acid sequence of human-originated soluble
20 thrombomodulin
22 <400> SEQUENCE: 1
23 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
E--> 24 1 5 5 10 10 15
25 Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
E--> 26 20 20 25 25 30
27 His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
E--> 28 35 40 45
29 Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
E--> 30 50 55 60
31 Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
E--> 32 65 70 75
33 Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
E--> 34 85 90 95
35 Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
E--> 36 100 105 110
37 Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
E--> 38 115 120 125
39 Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
E--> 40 130 135 140
41 Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
E--> 42 145 150 155 160
43 Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg
E--> 44 165 170 175
45 Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Val Ser Ile Thr

pp1-6
Does Not Comply
Corrected Diskette Needed

*misaligned
amino acid numbers
45 (see
item 3
on Error
summary
sheet)*

80

see p. 2

RAW SEQUENCE LISTING

DATE: 07/23/2004

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TIME: 15:23:45

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07232004\J501671.raw

E--> 46 180 185 190 *same*
 47 Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro
 E--> 48 195 200 205 *error*
 49 Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
 E--> 50 210 215 220
 51 Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
 E--> 52 225 230 235 240
 53 Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
 E--> 54 245 250 255
 55 Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
 E--> 56 260 265 270
 57 Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
 E--> 58 275 280 285
 59 Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
 E--> 60 290 295 300
 61 Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
 E--> 62 305 310 315 320
 63 His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
 E--> 64 325 330 335
 65 Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
 E--> 66 340 345 350
 67 Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro
 E--> 68 355 360 365
 69 Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
 E--> 70 370 375 380
 71 Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
 E--> 72 385 390 395 400
 73 Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
 E--> 74 405 410 415
 75 Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
 E--> 76 420 425 430
 77 Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
 E--> 78 435 440 445
 79 Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
 E--> 80 450 455 460
 81 Ile Cys Gly Pro Asp Ser Ala Leu Val Arg His Ile Gly Thr Asp Cys
 E--> 82 465 470 475 480
 83 Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
 E--> 84 485 490 495
 85 Pro Ser Pro Thr Pro Gly Ser Thr Leu Thr Pro Pro Ala Val Gly Leu
 E--> 86 500 505 510
 87 Val His Ser Gly
 E--> 88 515
 90 <210> SEQ ID NO: 2
 91 <211> LENGTH: 1548 *1547 (p.3)*
 92 <212> TYPE: DNA
 93 <213> ORGANISM: Artificial sequence
 95 <220> FEATURE:
 96 <223> OTHER INFORMATION: Partial base sequence of human-originated soluble

RAW SEQUENCE LISTING

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TIME: 15:23:45

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07232004\J501671.raw

97 thrombomodulin gene

99 <400> SEQUENCE: 2

```

100 atgcttggggg tcctgggtcct tggcgcgctg gccctggccg gcctgggggtt ccccgcaccc 60
101 gcagagccgc agccgggtgg cagccagtgc gtgcagcacg actgcttcgc gctctacccg 120
102 ggccccgcga ccttcctcaa tgccagtcag atctgcgacg gactgcgggg ccacctaatg 180
103 acagtgcgct cctcggtggc tgccgatgtc atttccttgc tactgaacgg cgacggcggc 240
104 gttggccgcc ggcgctctg gatcgccctg cagctgccac ccggtgcgg cgaccccaag 300
105 cgctcgggc cctgcgcgg cttccagtgg gttacgggag acaacaacac cagctatagc 360
106 aggtgggcac ggctcgacct caatggggct cccctctgcg gccggttggt cgctgctgtc 420
107 tccgctgtg aggccactgt gccagcgag ccgatctggg aggagcagca gtgcgaagtg 480
108 aaggccgatg gcttcctctg cgagttccac tcccagcca cctgcaggcc actggctgtg 540
109 gagcccgccg ccgcggctgc cgccgtctcg atcacctacg gcaccccggt cgcgggccgc 600
110 ggagcggact tccaggcgct gccgggtggc agctccgccc cggtgggtcc cctcggttta 660
111 cagctaattg gcaccgcgc gcccgagcgc gtccaggggc actgggcccag ggaggcgccg 720
112 ggcgcttggg actgcagcgt ggagaacggc ggctgcgagc acgctgcaa tgcgatccct 780
113 ggggctcccc gctgccagtg cccagccggc gccgcctgc aggcagacgg gcgctcctgc 840
114 accgcatccg cgacgcagtc ctgcaacgac ctctgcgagc acttctgcgt tcccaacccc 900
115 gaccagccgg gctcctactc gtgcatgtgc gagaccggct accggctggc ggccgaccaa 960
116 caccggtgcg aggacgtgga tgactgcata ctggagccca gtccgtgtcc gcagcgctgt 1020
117 gtcaacacac aggggtggctt cgagtggcac tgctacccta actacgacct ggtggacggc 1080
118 gagtgtgtgg agcccgtgga cccgtgcttc agagccaact gcgagtacca gtgccagccc 1140
119 ctgaacaaaa ctagctacct ctgctctgc gccgagggt tgcgcgccat tccccacgag 1200
120 ccgcacaggt gccagatgtt ttgcaaccag actgctgtc cagccgactg cgaccccaac 1260
121 acccaggcta gctgtgagtg cctgaaggc tacatcctgg acgacggtt catctgcacg 1320
122 gacatcgacg agtgcgaaaa cggcggcttc tgctccgggg tgtgccacaa cctccccgtt 1380
E--> 123 accttcgagt gcatctgcgg gcccgactcg gcccttgtec gccacattgg caccgacg 1440/1439
E--> 124 gactccggca aggtggacgg tggcgacagc ggctctggcg agccccgcc cagcccgacg 1500/1499
E--> 125 cccggctcca ccttgactcc tccggccgtg gggctcgtgc attcgggc 1547 1548
127 <210> SEQ ID NO: 3
128 <211> LENGTH: 132
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Partial amino acid sequence of human-originated soluble
134 thrombomodulin
E--> 136 <400> SEQUENCE: 8 3 ← change to
137 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Gly Leu Gly
E--> 138 1 5 10 15
139 Phe Pro Asp Pro Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro
E--> 140 20 25 30
141 Leu Asn Gln Thr Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro
E--> 142 35 40 45
143 Ile Pro His Glu Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala
E--> 144 50 55 60
145 Cys Pro Ala Asp Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro
E--> 146 65 70 75 80
147 Glu Gly Tyr Ile Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu
E--> 148 85 90 95
149 Cys Glu Asn Gly Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly

```

FYI:
periods
are
invalid
nucleic
acid
designators

This is a
group of 9 positions,
not 10.

misaligned amino acid numbers
see p. 4

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/501,671

DATE: 07/23/2004

TIME: 15:23:45

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07232004\J501671.raw

*misaligned
number*

```

E--> 150          100          105          110
      151 Thr Phe Glu Cys Ile Cys Gly Pro Asp Ser Ala Leu Val Arg His Ile
E--> 152          115          120          125
      153 Gly Thr Asp Cys
E--> 154          130
      174 <210> SEQ ID NO: 5
      175 <211> LENGTH: 516
      176 <212> TYPE: PRT
      177 <213> ORGANISM: Artificial sequence
      179 <220> FEATURE:
      180 <223> OTHER INFORMATION: Partial amino acid sequence of human-originated soluble
      181 thrombomodulin
      183 <400> SEQUENCE: 5
      184 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
E--> 185 1          5          10          15
      186 Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
E--> 187          20          25          30
      188 His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
E--> 189          35          40          45
      190 Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
E--> 191          50          55          60
      192 Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
E--> 193 65          70          75          80
      194 Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Gly Cys
E--> 195          85          90          95
      196 Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
E--> 197          100          105          110
      198 Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
E--> 199          115          120          125
      200 Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
E--> 201          130          135          140
      202 Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
E--> 203 145          150          155          160
      204 Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg
E--> 205          165          170          175
      206 Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Val Ser Ile Thr
E--> 207          180          185          190
      208 Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro
E--> 209          195          200          205
      210 Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
E--> 211          210          215          220
      212 Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
E--> 213 225          230          235          240
      214 Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
E--> 215          245          250          255
      216 Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
E--> 217          260          265          270
      218 Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
E--> 219          275          280          285

```

*misaligned
amino acid
number**P.5*

RAW SEQUENCE LISTING

DATE: 07/23/2004

PATENT APPLICATION: US/10/501,671

TIME: 15:23:45

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07232004\J501671.raw

same error

```

220 Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
E--> 221      290                      295                      300
222 Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
E--> 223 305                      310                      315                      320
224 His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
E--> 225                      325                      330                      335
226 Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
E--> 227                      340                      345                      350
228 Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro
E--> 229                      355                      360                      365
230 Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
E--> 231                      370                      375                      380
232 Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
E--> 233 385                      390                      395                      400
234 Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
E--> 235                      405                      410                      415
236 Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
E--> 237                      420                      425                      430
238 Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
E--> 239                      435                      440                      445
240 Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
E--> 241                      450                      455                      460
242 Ile Cys Gly Pro Asp Ser Ala Leu Ala Arg His Ile Gly Thr Asp Cys
E--> 243 465                      470                      475                      480
244 Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
E--> 245                      485                      490                      495
246 Pro Ser Pro Thr Pro Gly Ser Thr Leu Thr Pro Pro Ala Val Gly Leu
E--> 247                      500                      505                      510
248 Val His Ser Gly
E--> 249                      515
288 <210> SEQ ID NO: 7
289 <211> LENGTH: 132
290 <212> TYPE: PRT
291 <213> ORGANISM: Artificial sequence
W--> 292 <220> FEATURE:
293 <223> OTHER INFORMATION: Partial amino acid sequence of human-originated soluble
294      thrombomodulin
296 <400> SEQUENCE: 7
297 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
E--> 298 1      5                      10                      15
299 Phe Pro Asp Pro Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro
E--> 300      20                      25                      30
301 Leu Asn Gln Thr Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro
E--> 302      35                      40                      45
303 Ile Pro His Glu Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala
E--> 304      50                      55                      60
305 Cys Pro Ala Asp Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro
E--> 306 65                      70                      75                      80
307 Glu Gly Tyr Ile Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu

```

misaligned amino acid numbers
P.6

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 07/23/2004

PATENT APPLICATION: US/10/501,671

TIME: 15:23:46

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07232004\J501671.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 32

Seq#:3; Line(s) 146

Seq#:4; Line(s) 172

Seq#:7; Line(s) 306

Seq#:8; Line(s) 332

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/501,671

DATE: 07/23/2004

TIME: 15:23:46

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07232004\J501671.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:24 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1 /
M:332 Repeated in SeqNo=1
L:123 M:254 E: No. of Bases conflict, LENGTH:Input:1440 Counted:1439 SEQ:2 ✓
L:123 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓
M:254 Repeated in SeqNo=2
L:125 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1548 Found:1547 SEQ:2 ✓
L:136 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:8 ✓
L:138 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8 ✓
M:332 Repeated in SeqNo=3
L:185 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5 ✓
M:332 Repeated in SeqNo=5
L:292 M:283 W: Missing Blank Line separator, <220> field identifier
L:298 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7 ✓
M:332 Repeated in SeqNo=7
L:349 M:254 E: No. of Bases conflict, LENGTH:Input:12 Counted:22 SEQ:9 ✓
L:349 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 ✓
L:349 M:252 E: No. of Seq. differs, <211> LENGTH:Input:21 Found:22 SEQ:9